

# High-quality kākāpō population sequencing provides breakthrough in understanding key conservation genetics

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Kākāpō in burrow. Credit: Jake Osborne

High-quality sequencing of nearly the entire kākāpō population is helping New Zealand to manage the health of this critically endangered

species.

Not only is it already making a difference to kākāpō survival, but establishing sequencing methods to work with populations under threat is also likely to be the foundation for the future of endangered wildlife science in New Zealand and the rest of the world.

The state-of-the-art methods developed by Dr. Joseph Guhlin (University of Otago) and an international team to study kākāpō has revealed important aspects of kākāpō biology. The methods, reusable code, and pipeline is a blueprint and tool for conservation genomics in other species, especially intensively managed species. The research results have been published in *Nature Ecology and Evolution*.

Dr. Guhlin's work over the last year had two very significant outcomes. First, it makes available an in-depth understanding of kākāpō biology that simply would not be possible without genomics. And second, it provides a high-quality code and reusable pipeline—allowing other researchers to rapidly integrate these methods into their own work—which has significantly advanced New Zealand's genomic capability.

This has given researchers the tools needed to identify specific genetic characteristics that are crucial to survival.

"Using technology created by Google, we have achieved what is likely the highest quality variant dataset for any [endangered species](#) in the world. This dataset is made available, through DOC and Ngai Tahu, for future researchers working with kākāpō," Dr. Guhlin said.

Department of Conservation's Science Advisor for Kākāpō Recovery, Dr. Andrew Digby, believes the [genetic tools](#) this study provides will make an immense difference to kākāpō conservation.

"Kākāpō suffer from disease and low reproductive output, so by understanding the genetic reasons for these problems, we can now help mitigate them. It gives us the ability to predict things like kākāpō chick growth and susceptibility to disease, which changes our on-the-ground management practices and will help improve survival rates."

While the study marks the beginning of a new era of kākāpō conservation genetics, Dr. Digby acknowledges what it means for the future of all threatened species.

"The Kakapo125+ project is a great example of how [genetic data](#) can assist population growth. The novel genetic and machine learning tools developed can be applied to improve the productivity and survival of other taonga under conservation management."

**More information:** Joseph Guhlin et al, Species-wide genomics of kākāpō provides tools to accelerate recovery, *Nature Ecology & Evolution* (2023). [DOI: 10.1038/s41559-023-02165-y](https://doi.org/10.1038/s41559-023-02165-y)

Provided by University of Otago

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